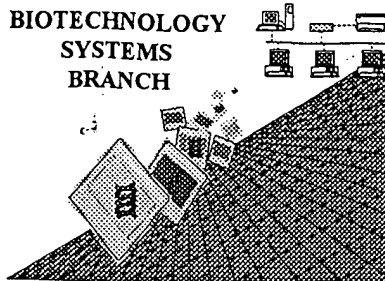


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/830,111
Source: Pct/09
Date Processed by STIC: 8/30/2001

54
#6

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/830,111
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>Wrapped Nucleics Wrapped Aminos</u>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>Misaligned Amino Numbering</u>	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,111

DATE: 08/30/2001
TIME: 11:37:14

Input Set : A:\ES.txt
Output Set: N:\CRF3\08302001\I830111.raw

Does Not Comply
Corrected Diskette Needed

OK
3 <110> APPLICANT: Kaneka Corporation
5 <120> TITLE OF INVENTION: Process for producing coenzyme Q10
7 <130> FILE REFERENCE: T549/QX-GT2
8 <140> CURRENT APPLICATION NUMBER: US/09/830,111
8 <141> CURRENT FILING DATE: 2001-07-23
8 <150> PRIOR APPLICATION NUMBER: JP P1999-237561
9 <151> PRIOR FILING DATE: 1999-08-24
W--> 10 <160> NUMBER OF SEQ ID: 2

ERRORED SEQUENCES

W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1653
13 <212> TYPE: DNA
14 <213> ORGANISM: Saioella complicata
W--> 15 <400> SEQUENCE: 1
E--> 17 20 ttttgtgggg tcgaaaagtc ggcacgggtg caggttcggc ttgagaccag taaaggctcg 60
19 gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120
21 aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169
W--> 23 25 Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser
W--> 25 1 5 10
E--> 28 2
30 tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217
31 Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser
W--> 32 20 25
E--> 33 5
E--> 34 gca cct tca tta cga cta aga tgt acc cog acg ago cgg cca tcg agt 265
35 Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser
W--> 36 30 35 40
E--> 38 10 tca tgg get get get gtg tct tcg gcg tcg aga ctg gtt gag cct gat 313
W--> 39 Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
W--> 40 45 50 55 60
42 ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361
W--> 43 15 Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met
W--> 44 65 70 75
45 tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409
46 Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro
W--> 47 20 80 85 90
E--> 49 tct ctc gac act gtc get aaa tac tat gtt cag tct gag gga aag cat 457
50 Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His
W--> 51 95 100 105
E--> 52 25
E--> 53 att cgt cog ctc atg gta ctg ctg atg get cag gcg acg gag gtt gcg 505
E--> 57 3
59 Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala
W--> 60 110 115 120

see following pages
for explanation -

many
errors

Please
consult
sequence
Rules
for valid
format

09/830,111 2

~~Sequence listing~~

<110> Kaneka Corporation

(5) <120> Process for producing coenzyme Q10

<130> T549/QX-GT2

<150> JP P1999-237561

<151> 1999-08-24

<160> 2

<210> 1

<211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

(20) ttttgtgggg tcgaaaagtc ggcacgggtg caggttcggc ttgagaccag taaaggctcg 60

gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169

(25) Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser

DO NOT use TAB codes.
amino acids MUST be
directly under
respective
codons.

1 5 10

misaligned nos. - see item 3
on Enr form may
that

(2)

tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217
Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser

misaligned

20

25

invalid nucleic acid designator

gca cct tca tta cga cta aga tgt acc cgg acg agc cgg cca tcg agt 265
Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser

30

35

40

(10) tca tgg get get get invalid tct tcg gcg tcg aga ctg gtt gag cct gat 313
Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp

45 50 55

60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361

(15) Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met

65 70 75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409

(20) Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro

80

85

90

tct ctc gac act gtc get invalid aaa tac tat gtt cag tct gag gga aag cat 457

Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His

95

100

105

(25)

att cgt do ctc atg gta ctg ctg atg get invalid cag gcg acg gag gtt gcg 505

invalid

invalid

(3)

delete
ALL
line
numbers

09/830,111 3

Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala

110 115 120

misaligned

cca aaa gtt cag ggt tgg gag aag gtc gtg gag gtt ccg gtg aac gag 553
Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu
125 130 135 140

gga ctc gca cca cca gag gtg ctc aat gac aag aac cca gat atg atg 601
Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met

145 150 155

aac atg agg tca gga cca tta acg aag gac ggc gag atc gag gga cag 649
Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln

160 165 170

acg tcg aat atc ctc gcc tcg caa cgg cgg ttg get gag atc acg gag 697
Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu
175 180 185

atg atc cat gca gca tca ctc ctc cac gac gac gtt atc gac get tcc 745
Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser
190 195 200

invalid

gag acc aga cga aac gca cca tcc gga aac cag gca ttc gga aac aag 793
Glu Thr Arg Arg Am Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys

205 210 215 220

4

atg gcg att ttg get ggt gat ttc ttg ttg gga cgg gcg tct gtt gca 841
Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala

225 230 235

ttg gcg agg ttg cgc aat ccg gag gtg att gag ctt ttg get act gtt 889
Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val
240 245 250

att gca aac ttg gtt gag gga gag ttc atg cag ttg aaa aat act gtt 937
Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val
255 260 265

gat gat gcg att gag get acg gcg acg cag gaa acg ttc gat tac tat 985
Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr

270 275 280

ttg cag aag act tac ttg aag act gcg tcc ttg att gcc aag tcg tgc 1033
Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
285 290 295 300

aga gca agt gcg ctt get ggt ggt get acg get gag gtt get gat get 1081
Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala
305 310 315

get tat get tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac 1129

move amino acids directly under codons

5

Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp
 320 325 330 *misaligned*

gac atg ctc gac tac acc gtc tcc ggt acc gac ctc ggt aag ccc gcc 1177
 5 ← Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala
move over 335 340 345

ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca 1225
 Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala
lower-case letters

10 350 355 360

tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct 1273
 Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser
 365 370 375 380

15

gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat 1321
 Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp
 385 390 395

20 gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg 1369
 Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala
 400 405 410

ttg gat gca att cgg acg ttc ccg gag agt gca cgg aag ggt ttg 1417
 25 ← Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu
 415 420 425

6

gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcgagct 1467
 Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg
 430 435 440

5

cggtaccggt ggatcctcta gagtcgacct gcaggcatgc aagcttggct gttttggcgg 1527

atgagagaag attttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587

10 acagaatttg cctggcggca gtagcgcggt ggtccacct gaccccatgc cgaactcaga 1647

agtgaa

1653

15 <210> 2
 <211> 440
 <212> PRT

delete

<213> Saioella complicata

20 <400> 2

Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser Ser Arg Ser

insert a space after each group of 10 bases

1653 see item 1 on Enr summary sheet

15 1 5 10 *misaligned*
 Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro
 20 25

30
 25 Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser
 35 40
 45

Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
 50 55 60

Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu
 65 70 75

5 Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly
 80 85 90

His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu
 95 100 105

Gly Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala
 10 110 115 120

Thr Glu Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu
 125 130 135

Val Pro Val Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp
 140 145 150

15 Lys Asn Pro Asp Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys
 155 160 165

Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln
 170 175 180

Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala Ala Ser Leu
 20 185 190 195

Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg Asn Ala
 200 205 210

Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu Ala
 215 220 225

09/230,111

6

25 Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu

230 235 240

Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn

245 250 255

Leu Val Glu Gly Glu Phe Met Gin Leu Lys Asn Thr Val Asp Asp

260 265 270

Ala Ile Glu Ala Thr Ala Thr Gin Glu Thr Phe Asp Tyr Tyr Leu

275 280 285

Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys

290 295 300

Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp

305 310 315

Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gin Ile

320

325

330

Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly

335 340 345

Lys Pro Ala Gly Ala Asp Leu Gin Leu Gly Leu Ala Thr Ala Pro

350 355 360

Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile

365

370

375

Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu

380

385

390

Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala

395

400

405

Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro

410

415

420

25 Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val

425 430 435

Leu Thr Arg Ser Arg

440

dashes not permitted
invalid

delete extra spaces

delete extra spaces